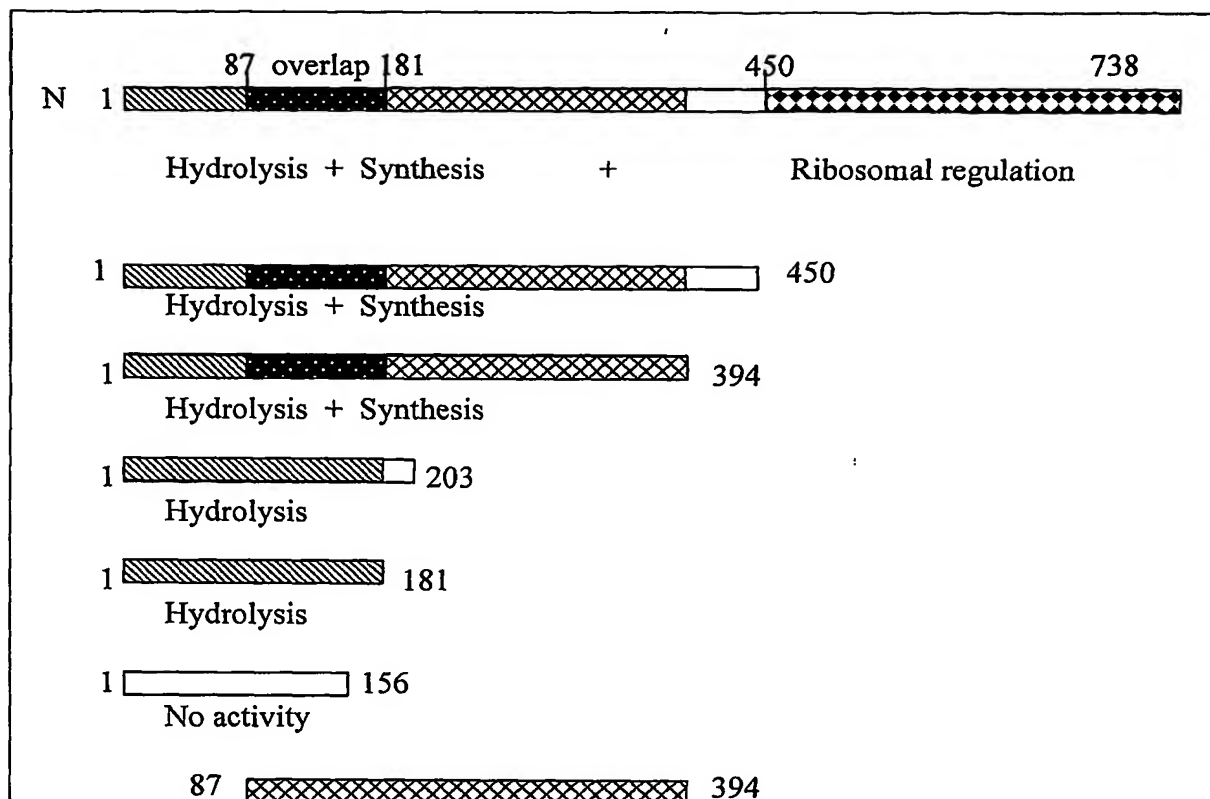


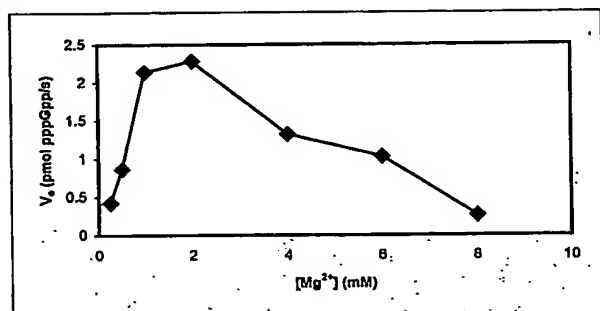
1/6
Figure 1



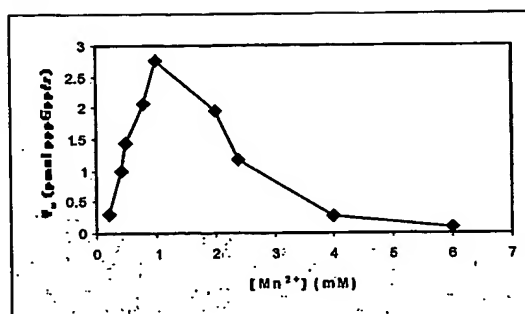
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FIGURE 2

A



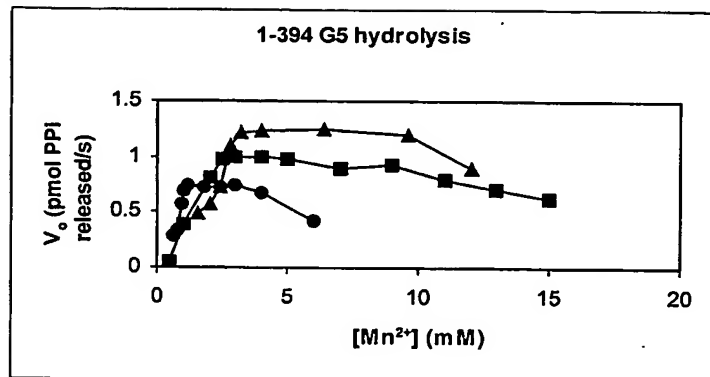
B



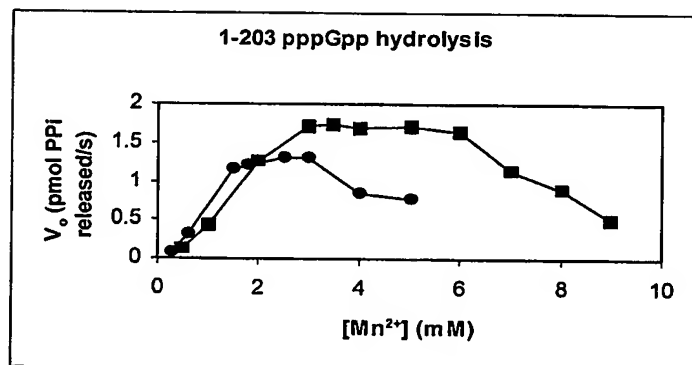
3/6

FIGURE 3

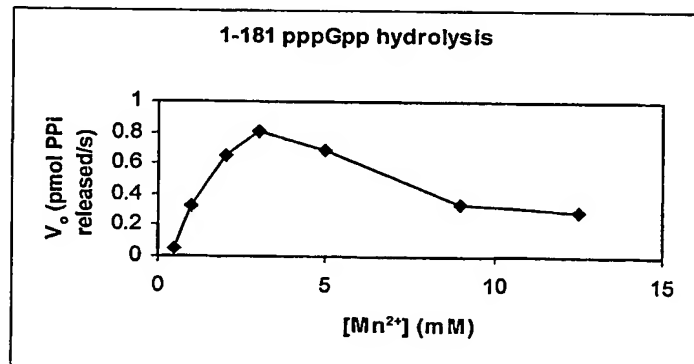
A



B



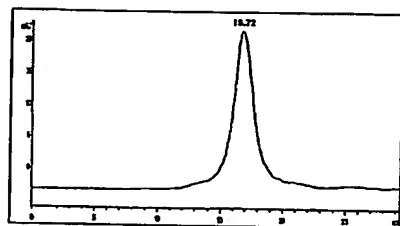
C



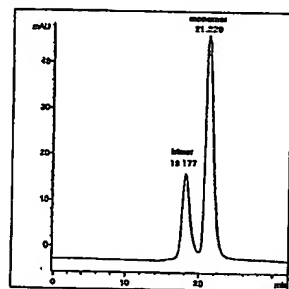
4/6

FIGURE 4

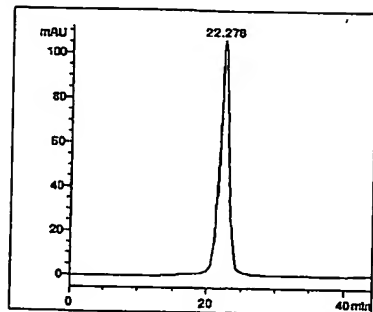
A



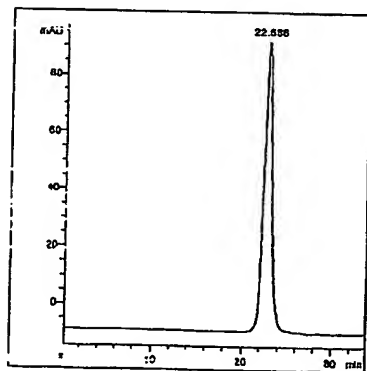
B



C.



D



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Figure 5

<p>A</p> <p>80HD81 G241 H344 m1 m2 C607 632DC633</p> <p>1 HD domain TGS ACT 738</p> <p>449 535 547 676</p>	<ul style="list-style-type: none"> •TGS 396-459 (21) •ACT 661-734 (22) •m1 (413-442), m2 (481-514), m3 (634-651) motifs •449-535 & 547-676 multimer area (20) •C607, D632, C633 multimer residues (16) •449-C term. ribosome binding (20) 	
<p>B</p> <p>80HD81 G241 H344</p> <p>1 450</p>	<p>Synthesis & Hydrolysis</p>	<ul style="list-style-type: none"> •G241 and H344 for probable nucleotide binding (16) •HD domain and doublet (13)
<p>C</p> <p>80HD81 G241 H344</p> <p>1 394</p>	<p>Synthesis & Hydrolysis</p>	<ul style="list-style-type: none"> •G241 and H344 for probable nucleotide binding (16) •HD domain and doublet (13)
<p>D</p> <p>80HD81</p> <p>1 203</p>	<p>Hydrolysis</p>	<ul style="list-style-type: none"> •HD domain and doublet (13) •Lacks probable ATP and GTP binding sites
<p>E</p> <p>80HD81</p> <p>1 181</p>	<p>Hydrolysis</p>	<ul style="list-style-type: none"> •HD domain and doublet (13) •Lacks probable ATP and GTP binding sites
<p>F</p> <p>80HD81</p> <p>1 156</p>	<p>No detectable activity</p>	<ul style="list-style-type: none"> •HD doublet present but HD domain disrupted
<p>G</p> <p>87 G241 H344 394</p>	<p>Synthesis</p>	<ul style="list-style-type: none"> •No HD doublet and disrupted HD domain •G241 and H344 for probable ATP and GTP binding (16)

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FIGURE 6

